Study of Long Noncoding RNA FER1L4 and RB1, as Its Competing Endogenous RNA Network Target Gene, in Breast Cancer

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Abstract

Introduction: Breast cancer is the second most common cause of cancer-related death among females, which requires an exploration for markers to propose a more specific categorization of this cancer. Long noncoding RNAs (lncRNAs), the main subset of noncoding transcripts, are involved in tumorigenic processes. In this study, we investigated the expression of the fer-1-like family member 4 (FER1L4) lncRNA and its competitive endogenous RNA network target gene, RB transcriptional corepressor 1 (RB1), in ductal carcinoma (invasive and in situ) tissue and its adjacent noncancerous tissue (ANCT). Furthermore, associations of FER1L4 and RB1 with various clinical features of the patients were analyzed.

Methods: Quantitative real-time PCR was used to measure the expression of the mentioned genes in 61 samples of ductal carcinoma and their ANCTs, and the data were analyzed using ANOVA and t tests.

Results: FER1L expression was not significantly different in breast tumor samples compared with their ANCT samples, while RB1 showed significant downregulation in tumor tissues (P = 0.008). In addition, increased expression of FER1L4 and decreased RB1 expression were significantly correlated with lymph node metastasis in breast cancer patients (P < 0.05).

Conclusion: FER1L4 is not upregulated in breast cancer tissue. However, RB1 expression is significantly downregulated.

Keywords: lncRNA FER1L4, Breast Cancer, RB1, ceRNA Network